

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/443,982DATE: 11/14/95
TIME: 16:09:01

INPUT SET: S7227.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: DIXIT, VISHVA M.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
FAS-ASSOCIATED APOPTOSIS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Morrison & Foerster

(B) STREET: 755 Page Mill Road

(C) CITY: Palo Alto

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/443,982

(B) FILING DATE: 18-MAY-1995

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Konski, Antoinette F.

(B) REGISTRATION NUMBER: 34,202

(C) REFERENCE/DOCKET NUMBER: 20344-21070.20

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415)813-5600

(B) TELEFAX: (415)494-0792

(C) TELEX: 706141 MRSNFOERS SFO

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1642 base pairs

(B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49
50 (ii) MOLECULE TYPE: cDNA
51
52
53 (ix) FEATURE:
54 (A) NAME/KEY: CDS
55 (B) LOCATION: 130..756
56
57 (ix) FEATURE:
58 (A) NAME/KEY: misc_feature
59 (B) LOCATION: 4..6
60 (D) OTHER INFORMATION: /note= "An in-frame stop codon 130
61 base pairs upstream of the initiator methionine"
62
63 (ix) FEATURE:
64 (A) NAME/KEY: polyA_signal
65 (B) LOCATION: 1636..1641
66 (D) OTHER INFORMATION: /note= "Potential poly(A)
67 adenylation signal"
68
69 (ix) FEATURE:
70 (A) NAME/KEY: misc_feature
71 (B) LOCATION: 198..753
72 (D) OTHER INFORMATION: /note= "Clone-15, 5' end of FADD"
73
74 (ix) FEATURE:
75 (A) NAME/KEY: misc_feature
76 (B) LOCATION: 249..753
77 (D) OTHER INFORMATION: /note= "Clone-8, 5' end of FADD"
78
79 (ix) FEATURE:
80 (A) NAME/KEY: misc_feature
81 (B) LOCATION: 177..658
82 (D) OTHER INFORMATION: /note= "Death Domain of FADD"
83
84 (ix) FEATURE:
85 (A) NAME/KEY: mutation
86 (B) LOCATION: replace(490..492, "")
87 (D) OTHER INFORMATION: /note= "For FADDmt, the sequence is
88 altered to either AAT or AAC and the corresponding codon from
89 Val to Asn"
90
91 (ix) FEATURE:
92 (A) NAME/KEY: misc_feature
93 (B) LOCATION: group(250..753, 232..753)
94 (D) OTHER INFORMATION: /note= "Corresponding amino acids
95 can comprise C-terminal polypeptide fragments of FADD"
96
97 (ix) FEATURE:
98 (A) NAME/KEY: misc_feature
99 (B) LOCATION: 253..753

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100 (D) OTHER INFORMATION: /note= "Corresponding amino acids
101 can comprise a polypeptide fragment of FADD designated NFD-2"
102
103 (ix) FEATURE:
104 (A) NAME/KEY: misc_feature
105 (B) LOCATION: 310..753
106 (D) OTHER INFORMATION: /note= "Corresponding amino acids
107 can comprise a polypeptide fragment of FADD designated NFD-3"
108
109 (ix) FEATURE:
110 (A) NAME/KEY: misc_feature
111 (B) LOCATION: 367..753
112 (D) OTHER INFORMATION: /note= "Corresponding amino acids
113 can comprise polypeptide fragment of FADD designated NFD-4"
114
115 (ix) FEATURE:
116 (A) NAME/KEY: misc_feature
117 (B) LOCATION: 131..504
118 (D) OTHER INFORMATION: /note= "Corresponding amino acids
119 can comprise an N-terminal half polypeptide fragment of FADD"
120
121 (ix) FEATURE:
122 (A) NAME/KEY: misc_feature
123 (B) LOCATION: 71..478
124 (D) OTHER INFORMATION: /note= "Corresponding amino acids
125 can comprise an N-terminal half polypeptide fragment of FADD
126 designated N-FADD"
127
128 (ix) FEATURE:
129 (A) NAME/KEY: misc_feature
130 (B) LOCATION: 133..501
131 (D) OTHER INFORMATION: /note= "Corresponding amino acids
132 can comprise an N-terminal half polypeptide fragment of FADD"
133
134
135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
136
137 CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG 60
138
139 GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA 120
140
141 GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC 168
142 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser
143 1 5 10
144
145 AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG 216
146 Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly
147 15 20 25
148
149 CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC 264
150 Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
151 30 35 40 45
152

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153	TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG	312
154	Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu	
155	50 55 60	
156		
157	CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG	360
158	Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg	
159	65 70 75	
160		
161	CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG	408
162	Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly	
163	80 85 90	
164		
165	GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG	456
166	Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly	
167	95 100 105	
168		
169	AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG	504
170	Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys	
171	110 115 120 125	
172		
173	ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG	552
174	Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val	
175	130 135 140	
176		
177	CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA	600
178	Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr	
179	145 150 155	
180		
181	GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG	648
182	Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val	
183	160 165 170	
184		
185	GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG	696
186	Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg	
187	175 180 185	
188		
189	AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC	744
190	Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser	
191	190 195 200 205	
192		
193	GAA GCG TCC TGA TGGGCCGCTG CTTTGCGCTG GTGGACCACA GGCATCTACA	796
194	Glu Ala Ser *	
195		
196		
197	CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA	856
198		
199	GCCAGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCGTT TATTAATGCC	916
200		
201	TCTCCCGCAC CAGGCCGGGC TTGGGCCCTG CACAGATATT TCCATTTCTT CCTCACTATG	976
202		
203	ACACTGAGCA AGATCTTGTC TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG	1036
204		
205	AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC	1096

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206
207 GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAAGC AGAGAGGTGG AGAACTGGGA 1156
208
209 TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTCAAC CACTGTGGCG TTCTGCTGCC 1216
210
211 CCTGCAGTTG GCAGAAAGGA TGT'TTTGTCC CATTTCCCTG GAGGCCACCG GGACAGACCT 1276
212
213 GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG 1336
214
215 GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCCTGTGT GAGTTGAGTC TCCTCTCTGA 1396
216
217 GACTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG 1456
218
219 CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCCTG 1516
220
221 CAATTCTACA GTTTCCTTACT GTTTTGTATC AAAATCACTA TCTTCTGAT AACAGAATTG 1576
222
223 CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCTAA GGTAATCCTA 1636
224
225 TTAAAA 1642
226
227

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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239 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
240 1 5 10 15
241
242 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
243 20 25 30
244
245 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
246 35 40 45
247
248 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
249 50 55 60
250
251 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
252 65 70 75 80
253
254 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
255 85 90 95
256
257 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
258 100 105 110

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
278	Stop Codon at end of sequence removed - no error	